-- Since it is preferable to mimic this distribution of amino acids, the invention provides a library wherein the distribution of amino acids at the positions to be varied mimics that seen in the antigen binding site of antibodies. Such bias in the substitution of amino acids that permits selection of certain polypeptides (not just antibody polypeptides) against a range of target ligands is easily applied to any polypeptide repertoire according to the invention. There are various methods of biasing the amino acid distribution at the position to be varied (including the use of tri-nucleotide mutagenesis, WO97/08320, Morphosys, supra), of which the preferred method, due to ease of synthesis, is the use of conventional degenerate codons. By comparing the amino acid profile encoded by all combinations of degenerate codons (with single, double, triple and quadruple degeneracy in equal ratios at each position) with the natural amino acid use it is possible to calculate the most representative codon. The codons (AGT)(AGC)T (SEQ ID NO: 3), (AGT)(AGC)C (SEQ ID NO: 4) and (AGT)(AGC)(CT) (SEQ ID NO: 5)– that is, DVT, DVC AND DVY, respectively using IUPAC nomenclature – are those closest to the desired amino acid profile: they encode 22% serine and 11% tyrosine, asparagine, glycine, alanine, aspartate, threonine and cysteine. Preferably, therefore, libraries are constructed using either the DVT, DVC or DVY codon at each of the diversified positions.--

· On page 24, replace the paragraph on lines 25 to 36 with the following replacement paragraph:

-- As stated above, polypeptides which make up antibody libraries according to the invention may be whole antibodies or fragments thereof, such as Fab, $F(ab')_2$, Fv or scFv fragments, or separate V_H or V_L domains, any of which is either modified or unmodified. Of these, single-chain Fv fragments, or scFvs, are of particular use. ScFv fragments, as well as other antibody polypeptides, are reliably generated by antibody engineering methods well known in the art. The scFv is formed by connecting the V_H and V_L genes using an oligonucleotide that encodes an appropriately designed linker peptide, such as $(Gly\text{-}Gly\text{-}Gly\text{-}Gly\text{-}Ser)_3$ (SEQ ID NO: 6) or equivalent linker peptide(s). The linker bridges the C-terminal end of the first V region and N-terminal end of the second V region, ordered as either V_H-linker-V_L or V_L-linker-V_H. In principle, the binding site of the scFv can faithfully reproduce the specificity of the corresponding whole antibody and vice-versa.--

· Replace Table 1 (pages 48-50) with the attached replacement Table 1 (now pages 48 and 49).